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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2007; month=12; day=20; hr=13; min=47; sec=13; ms=227;
]

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Reviewer Comments:

<210> 10

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> C-terminal portion of domain III of laminin gamma 2.

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1 5 10 15

Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe Gly Gly
20 25 30

Pro Asn Cys Glu His Gly Ala Phe Ser
35 40

Please remove the above "1," which appears at the end of the submmitted
file.

Application No: 10580101 Version No: 1.0

Input Set:

Output Set:

Started: 2007-11-29 13:01:31.530
Finished: 2007-11-29 13:01:33.052
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 522 ms
Total Warnings: 0
Total Errors: 8
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

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E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (10)

SEQUENCE LISTING

<110> Tryggvason, Karl
Salo, Sirpa

<120> Use of antibodies to the gamma 2 chain of laminin 5 to inhibit tumor growth and metastasis

<130> 02-1147

<140> 10580101

<141> 2007-11-29

<150> 60/422,009

<151> 2002-10-29

<150> US 09/756,071

<151> 2001-01-08

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 5200

<212> DNA

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<222> (118)..(183)

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atg cct gcg etc tgg ctg ggc tgc tgc etc tgc ttc tcg etc etc ctg 165

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu

1 5 10 15

ccc gca gcc cgg gcc acc tcc agg agg gaa gtc tgt gat tgc aat ggg 213

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20 25 30

aag tcc agg cag tgt atc ttt gat cgg gaa ctt cac aga caa act ggt 261

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35 40 45

aat gga ttc cgc tgc ctc aac tgc aat gac aac act gat ggc att cac 309

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Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg			
	100	105	110
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Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys			
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Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala			
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Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala			
145	150	155	160
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Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu			
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Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His			
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Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr			
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Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn			
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Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe			
225	230	235	240
agc tca gcc caa cga cta gat cct gtc tat ttt gtg gct cct gcc aaa			885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys			
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Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp			
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Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile			
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Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn	
305 310 315 320	
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Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr	
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Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys	
450 455 460	
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His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val	
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Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys	
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Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg	
500 505 510	

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Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser	
595 600 605	
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Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met	
610 615 620	
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625 630 635 640	
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Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu	
675 680 685	
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Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg	
690 695 700	
gtt cgg gct ctg gga agt cag tac cag aac cga gtt cgg gat act cac	2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His	
705 710 715 720	
agg ctc atc act cag atg cag ctg agc ctg gca gaa agt gaa gct tcc	2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser	
725 730 735	
ttg gga aac act aac att cct gcc tca gac cac tac gtg ggg cca aat	2373

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn	
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ggc ttt aaa agt ctg gct cag gag gcc aca aga tta gca gaa agc cac	2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His	
755	760 765
gtt gag tca gcc agt aac atg gag caa ctg aca agg gaa act gag gac	2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp	
770	775 780
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Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly	
785	790 795 800
gtc gga agc gga agc ggt agc ccg gac ggt gct gtg gtg caa ggg ctt	2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu	
805	810 815
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Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg	
820	825 830
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Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser	
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900	905 910
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915	920 925
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Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu	
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cag gtg gac aac aga aaa gca gaa gct gaa gaa gcc atg aag aga ctc	3045
Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu	

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Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln			
980	985	990	
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Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys			
995	1000	1005	
aat ggg gcc ggg gag gcc ctg gaa atc tcc agt gag att gaa cag			3186
Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln			
1010	1015	1020	
gag att ggg agt ctg aac ttg gaa gcc aat gtg aca gca gat gga			3231
Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly			
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gcc ttg gcc atg gaa aag gga ctg gcc tct ctg aag agt gag atg			3276
Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met			
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agg gaa gtg gaa gga gag ctg gaa agg aag gag ctg gag ttt gac			3321
Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp			
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acg aat atg gat gca gta cag atg gtg att aca gaa gcc cag aag			3366
Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys			
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Val Asp Thr Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr			
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Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met Asp Gln Pro Leu			
1100	1105	1110	
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Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln Lys Leu Ser			
1115	1120	1125	
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3729

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1190

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